

# Full wwPDB X-ray Structure Validation Report (i)

Jan 3, 2024 – 05:41 pm GMT

PDB ID : 5CPL

Title: The crystal structure of Xenobiotic reductase A (XenA) from Pseudomonas

putida in complex with a nicotinamide mimic (mNH2)

Authors: Knaus, T.; Paul, C.E.; Levy, C.W.; Mutti, F.G.; Hollmann, F.; Scrutton, N.S.

Deposited on : 2015-07-21

Resolution : 1.57 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

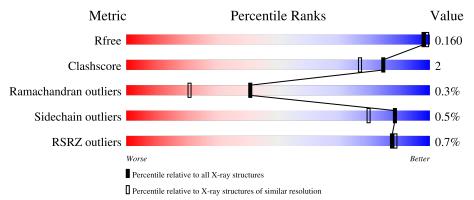
Validation Pipeline (wwPDB-VP) : 2.36

### 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.57 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
$R_{free}$	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain		
1	A	371	93%	•	-
1	В	371	91%	5%	-



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 12029 atoms, of which 5522 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called Xenobiotic reductase.

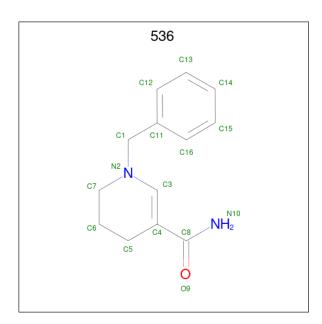
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	359	10001	C 1787	H 2718	N 502	O 507	S 7	0	3	0
1	В	359	Total 5542	_		N 502	O 510	S 7	0	5	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	364	ARG	-	expression tag	UNP Q9R9V9
A	365	PRO	-	expression tag	UNP Q9R9V9
A	366	HIS	-	expression tag	UNP Q9R9V9
A	367	HIS	-	expression tag	UNP Q9R9V9
A	368	HIS	-	expression tag	UNP Q9R9V9
A	369	HIS	-	expression tag	UNP Q9R9V9
A	370	HIS	-	expression tag	UNP Q9R9V9
A	371	HIS	-	expression tag	UNP Q9R9V9
В	364	ARG	-	expression tag	UNP Q9R9V9
В	365	PRO	-	expression tag	UNP Q9R9V9
В	366	HIS	-	expression tag	UNP Q9R9V9
В	367	HIS	-	expression tag	UNP Q9R9V9
В	368	HIS	-	expression tag	UNP Q9R9V9
В	369	HIS	-	expression tag	UNP Q9R9V9
В	370	HIS	-	expression tag	UNP Q9R9V9
В	371	HIS	-	expression tag	UNP Q9R9V9

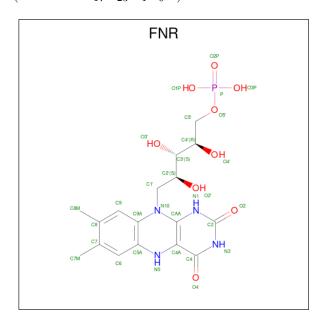
• Molecule 2 is 1-benzyl-1,4,5,6-tetrahydropyridine-3-carboxamide (three-letter code: 536) (formula:  $C_{13}H_{16}N_2O$ ).





Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
2	Λ	1	Total	С	Н	N	О	0	0
2	Α	1	32	13	16	2	1	U	U
2	D	1	Total	С	Н	N	О	0	0
2	Б	1	32	13	16	2	1	U	0

• Molecule 3 is 1-DEOXY-1-(7,8-DIMETHYL-2,4-DIOXO-3,4-DIHYDRO-2H-BENZO[G]P TERIDIN-1-ID-10(5H)-YL)-5-O-PHOSPHONATO-D-RIBITOL (three-letter code: FNR) (formula:  $C_{17}H_{23}N_4O_9P$ ).



Mol	Chain	Residues		Α	ton	ıs			ZeroOcc	AltConf
9	Λ	1	Total	С	Н	N	О	Р	0	0
)	A	1	52	17	21	4	9	1	U	0

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Mol	Chain	Residues		Α	tom	ıs			ZeroOcc	AltConf
9	D	1	Total	С	Н	N	О	Р	0	0
)	Б	1	52	17	21	4	9	1	0	0

• Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Ca 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	397	Total O 397 397	0	0
5	В	400	Total O 400 400	0	0



## 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants	56.80Å 83.82Å 155.88Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	47.02 - 1.57	Depositor
resolution (A)	53.37 - 1.57	EDS
% Data completeness	94.6 (47.02-1.57)	Depositor
(in resolution range)	94.1 (53.37-1.57)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.75  (at  1.57Å)	Xtriage
Refinement program	PHENIX dev_1977	Depositor
$R, R_{free}$	0.135 , $0.160$	Depositor
it, it free	0.136 , $0.160$	DCC
$R_{free}$ test set	5036 reflections $(4.92%)$	wwPDB-VP
Wilson B-factor $(\mathring{A}^2)$	14.7	Xtriage
Anisotropy	0.596	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.40, 50.4	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	12029	wwPDB-VP
Average B, all atoms $(Å^2)$	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 24.31 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.9310e-03.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

### 5 Model quality (i)

### 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, FNR, 536

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond	lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.44	0/2893	0.66	4/3944 (0.1%)	
1	В	0.45	0/2908	0.65	1/3964 (0.0%)	
All	All	0.44	0/5801	0.65	5/7908 (0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	302[A]	TRP	N-CA-C	5.30	125.31	111.00
1	A	302[B]	TRP	N-CA-C	5.30	125.31	111.00
1	A	302[A]	TRP	CB-CA-C	-5.16	100.08	110.40
1	A	302[B]	TRP	CB-CA-C	-5.16	100.08	110.40
1	В	296	LEU	CA-CB-CG	5.15	127.15	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	302[A]	TRP	Mainchain
1	A	302[B]	TRP	Mainchain



#### 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2803	2718	2719	11	0
1	В	2812	2730	2730	15	0
2	A	16	16	16	0	0
2	В	16	16	16	0	0
3	A	31	21	22	2	0
3	В	31	21	22	2	0
4	В	1	0	0	0	0
5	A	397	0	0	5	3
5	В	400	0	0	6	3
All	All	6507	5522	5525	26	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (26) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\text{\AA}) \end{array}$	Clash overlap (Å)
1:B:128[B]:GLU:OE2	5:B:502:HOH:O	1.94	0.84
1:A:246:GLU:OE1	5:A:501:HOH:O	2.01	0.78
1:B:76:ASP:OD1	1:B:166[A]:ARG:NH1	2.26	0.69
1:A:224:GLU:OE1	5:A:502:HOH:O	2.16	0.58
1:B:360:GLU:OE1	5:B:504:HOH:O	2.17	0.58
1:B:159:ASP:OD1	5:B:503:HOH:O	2.17	0.57
1:B:25:CYS:H	3:B:403:FNR:H5	1.52	0.57
1:A:25:CYS:H	3:A:402:FNR:H5	1.57	0.51
1:A:315:GLN:NE2	5:A:504:HOH:O	2.25	0.51
1:B:295:LYS:NZ	5:B:514:HOH:O	2.49	0.45
1:B:301:ALA:O	1:B:302[B]:TRP:CB	2.66	0.44
1:B:208[B]:SER:HB2	1:B:251:LEU:HD13	2.00	0.44
1:A:254[B]:ARG:NH2	5:A:516:HOH:O	2.50	0.43
1:A:243:GLN:NE2	5:A:523:HOH:O	2.52	0.43
1:A:302[B]:TRP:CD2	3:A:402:FNR:H5'1	2.54	0.43
1:A:15:LEU:HD23	1:A:95:VAL:HG21	2.02	0.42
1:B:301:ALA:O	1:B:302[B]:TRP:HB2	2.20	0.42
1:B:295:LYS:NZ	5:B:512:HOH:O	2.48	0.42

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COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Atom-1	Atom-2	Interatomic	Clash
7100111-1	1100111-2	distance (Å)	overlap (Å)
1:B:111[A]:ARG:NH1	5:B:517:HOH:O	2.52	0.42
1:B:180:ALA:HA	1:B:186:GLN:OE1	2.20	0.41
1:B:302[B]:TRP:CD2	3:B:403:FNR:H5'1	2.55	0.41
1:A:301:ALA:O	1:A:302[B]:TRP:CB	2.69	0.41
1:A:336:TYR:OH	1:A:340:LYS:HD2	2.21	0.40
1:B:15:LEU:HD23	1:B:95:VAL:HG21	2.03	0.40
1:B:83:VAL:HB	1:B:84:PRO:HD3	2.03	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
5:A:655:HOH:O	5:B:715:HOH:O[3_444]	2.13	0.07
5:A:888:HOH:O	5:B:865:HOH:O[3_444]	2.18	0.02
5:A:506:HOH:O	5:B:783:HOH:O[3_444]	2.19	0.01

#### 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles		
1	A	360/371 (97%)	346 (96%)	12 (3%)	2 (1%)	25 8		
1	В	$362/371 \ (98\%)$	348 (96%)	12 (3%)	2 (1%)	25 8		
All	All	$722/742 \ (97\%)$	694 (96%)	24 (3%)	4 (1%)	41 8		

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	302[A]	TRP
1	A	302[B]	TRP
1	В	302[A]	TRP
1	В	302[B]	TRP



#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Rotameric Outliers	
1	A	277/286 (97%)	275 (99%)	2 (1%)	84 72
1	В	279/286 (98%)	278 (100%)	1 (0%)	91 84
All	All	556/572 (97%)	553 (100%)	3 (0%)	88 80

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	118	HIS
1	A	178	HIS
1	В	178	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

#### 5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and



the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol Type		Chain	oin Dec	Res Link	Bond lengths			Bond angles		
$oxed{ \   Mol\                    $	Chain	Res	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
3	FNR	A	402	-	32,33,33	1.83	8 (25%)	40,50,50	1.02	2 (5%)
3	FNR	В	403	-	32,33,33	1.83	7 (21%)	40,50,50	1.00	0
2	536	A	401	-	17,17,17	2.90	6 (35%)	17,22,22	1.30	1 (5%)
2	536	В	401	-	17,17,17	2.87	6 (35%)	17,22,22	1.14	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FNR	A	402	-	-	1/18/18/18	0/3/3/3
3	FNR	В	403	-	-	1/18/18/18	0/3/3/3
2	536	A	401	-	-	0/7/18/18	0/2/2/2
2	536	В	401	-	-	0/7/18/18	0/2/2/2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
2	A	401	536	C13-C12	6.43	1.52	1.38
2	A	401	536	C16-C11	6.28	1.52	1.38
2	В	401	536	C13-C12	6.27	1.52	1.38
2	В	401	536	C16-C11	6.10	1.52	1.38
2	В	401	536	C15-C14	5.32	1.52	1.38
2	A	401	536	C15-C14	5.13	1.51	1.38
3	A	402	FNR	C4A-N5	4.53	1.45	1.35
3	A	402	FNR	CAA-N10	4.27	1.46	1.38
3	В	403	FNR	CAA-N10	4.19	1.46	1.38
3	В	403	FNR	C4-N3	-3.98	1.31	1.38
3	В	403	FNR	C4A-N5	3.70	1.43	1.35
2	A	401	536	C8-N10	3.53	1.42	1.33
2	В	401	536	C8-N10	3.50	1.42	1.33
3	В	403	FNR	C5A-N5	3.35	1.45	1.39
3	В	403	FNR	CAA-N1	-3.27	1.31	1.37
3	A	402	FNR	CAA-N1	-3.05	1.31	1.37
3	A	402	FNR	C9A-N10	2.96	1.46	1.41

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Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
3	В	403	FNR	C9A-N10	2.94	1.46	1.41
3	A	402	FNR	C4-N3	-2.87	1.33	1.38
3	A	402	FNR	C5A-C9A	-2.75	1.37	1.40
3	A	402	FNR	C5A-N5	2.71	1.44	1.39
3	В	403	FNR	C5A-C9A	-2.70	1.37	1.40
3	A	402	FNR	C2-N1	-2.54	1.33	1.37
2	A	401	536	C7-N2	-2.33	1.43	1.46
2	В	401	536	C3-N2	2.30	1.40	1.35
2	A	401	536	C3-N2	2.26	1.40	1.35
2	В	401	536	C7-N2	-2.16	1.43	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	401	536	C1-N2-C7	4.36	122.83	116.97
2	В	401	536	C1-N2-C7	4.04	122.40	116.97
3	A	402	FNR	C4-N3-C2	-2.74	122.40	126.34
3	A	402	FNR	O4-C4-C4A	-2.36	121.84	127.24

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	FNR	C4'-C5'-O5'-P
3	В	403	FNR	C4'-C5'-O5'-P

There are no ring outliers.

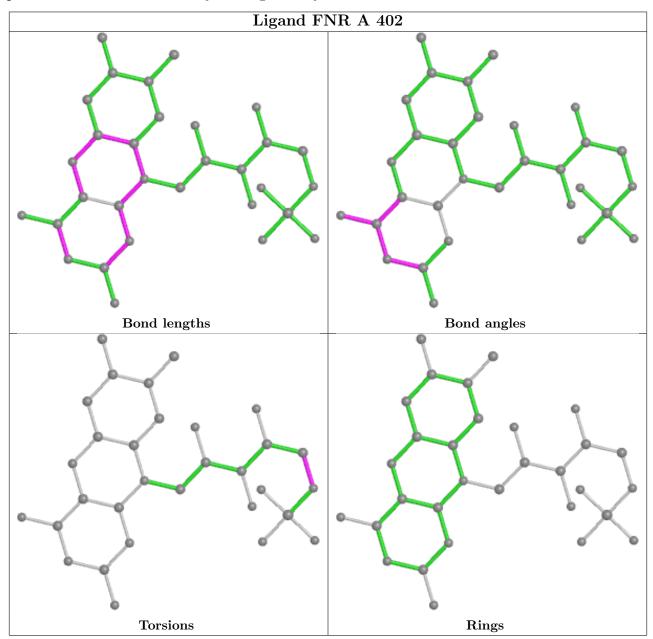
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	FNR	2	0
3	В	403	FNR	2	0

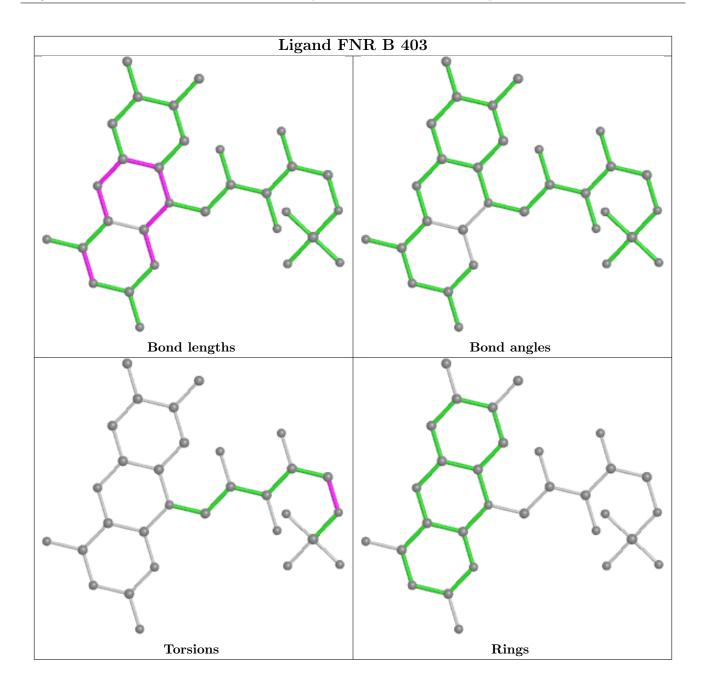
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the



average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







### 5.7 Other polymers (i)

There are no such residues in this entry.

### 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



### 6 Fit of model and data (i)

#### 6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median,  $95^{th}$  percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ $>$	# RSRZ > 2		$OWAB(A^2)$	Q<0.9
1	A	359/371 (96%)	-0.61	3 (0%)	86 87	11, 17, 28, 55	0
1	В	359/371 (96%)	-0.65	2 (0%)	89 90	11, 16, 28, 55	0
All	All	718/742 (96%)	-0.63	5 (0%)	87 88	11, 16, 28, 55	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	302[A]	TRP	4.4
1	В	302[A]	TRP	3.1
1	A	121	ALA	2.7
1	A	122	ASP	2.6
1	В	122	ASP	2.5

### 6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

#### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

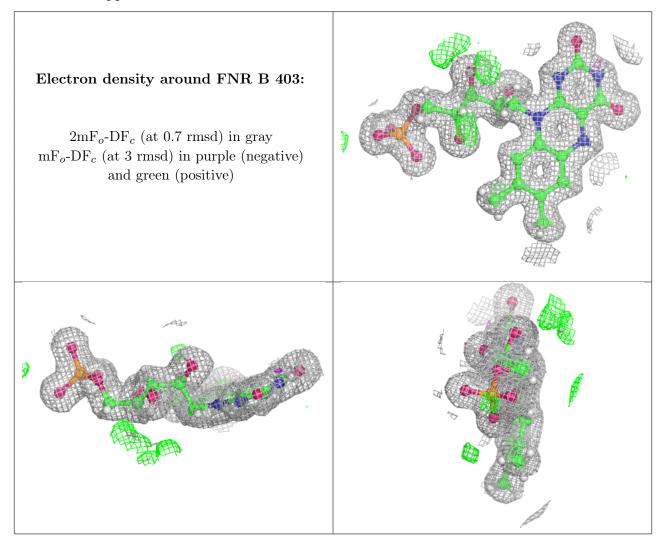
#### 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

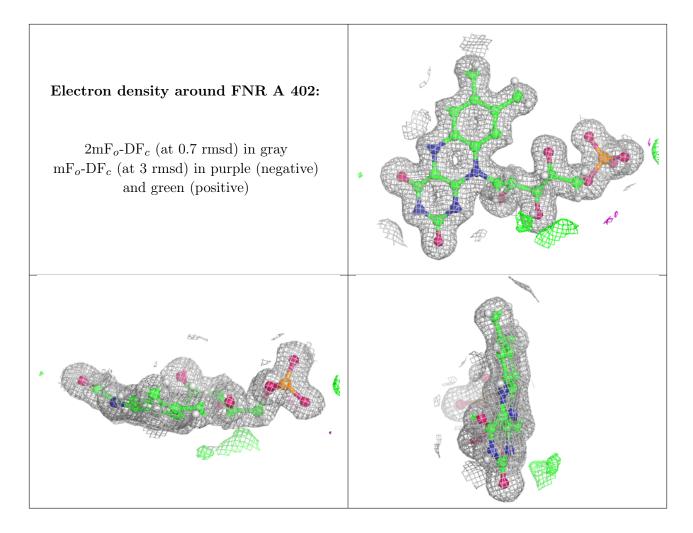


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	536	A	401	16/16	0.96	0.09	12,20,36,42	0
4	CA	В	402	1/1	0.96	0.07	35,35,35,35	0
2	536	В	401	16/16	0.97	0.09	11,22,39,42	0
3	FNR	В	403	31/31	0.99	0.05	9,12,16,17	0
3	FNR	A	402	31/31	0.99	0.05	10,13,17,17	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.







### 6.5 Other polymers (i)

There are no such residues in this entry.

